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SEQUENCE LISTINGS

SEQ ID NO	CLONE NAME	SEQUENCE
SEQ ID NO: 1	405 (pumilus)	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTTCGATGCCGTCAGCAAAGCCGCT GAACACAATCCAGTTATGGTTACGGTAT CGGAGGAGCTTCATACAATTTGCGGGATT AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCGGTGATTTGGGACAA GACAGGGACGAATTATAACAATGGCCCCT TATCACGATTGTGCAAAAGGTTAGACGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGTATGGGTGGCGCAACACACCTACTACA TAAAAAAATCTGGACGGCGGAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCGTTC GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAAAATTAGACGGTGCTAAAAACGCTAAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGGCCAAATACGAATTAA
SEQ ID NO: 2	406 (subtilis)	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCAGTCACATCGC TGTTCGTTGCAGCCGTCAGCAAAGCCGCT GAACACAATCCAGTCGTTATGGTTACGGTAT TGGAGGGCATTCATTTGCGGGATT AGAGCTATCTCGTATCTCAGGGCTGGCG GACAAGCTGTATGCAAGTTAGACGAA GACAGGCACAAATTATAACAATGGACCGTAT TACACGATTGTGCAAAAGGTTAGATGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGGGGCGCAACACACTTACTACA TAAAAAAATCTGGACGGCGGAATAAGTTGCA AACGTCGTAACGCTTGGCGCGAACCGTTC GACGACAGGCAAGGCCTCCGGGAACAGATC CAAATCAAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATAAATTACTT ATCAAGATTAGATGGTGCTAGAACGTTAAA TCCATGGCGTTGGACACATCGGCCTTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAAGAAGG GCTGAACGGCGGGGACTCAATACAAATTAG
SEQ ID NO: 3	402 (megaterium)	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTTCGATGCCGTCAGCAAAGCCGCT GAACACAATCCAGTTATGGTTACGGTAT

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		CGGAGGGAGCTTCATACAATTTGCAGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCGGTTGATTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTACTACA TAAAAAAATCTGGACGGCGGAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCGTT GACGACAAGCAAGGCCTCCGGAACAGATC CAAATCAAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTTCAAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGAGGACTAAATACAAATTAA
SEQ ID NO: 4	400 (lentus)	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTGGCGATGCGAGCCGTCAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACGGTAT CGGAGGGAGCTTCATACAATTTGCAGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCGGTTGATTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTACTACA TAAAAAAATCTGGACGGCGGAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCGTT GACGACAAGCAAGGCCTCCGGAACAGATC CAAATCAAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTTCAAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGGAGGACTAAATACAAATTAA
SEQ ID NO: 5	396 (circulans)	ATGAAATTATAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTGGCGATGCGAGCCGTCAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACGGTAT CGGAGGGAGCTTCATACAATTTGCAGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCGGTTGATTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCGAACACACTTACTACA

		TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCCTT GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGTATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTTCAAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAGAAGG ACTGAACGGCGGGGGCCTCAATACAAATTAA
SEQ ID NO: 6	392 (azotoformans)	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTGGCGATGCCGTCAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACGGTAT CGGAGGAGCTTCATACAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCGAGCTGTATCGGTTGATTTGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCAGAACACACTTACTACA TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCCTT GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGTATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTCACAA TTCATGGCGTTGGGCACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAGAAGG ACTGAACGGCGGGGGCCTAGATACAAATTAA
SEQ ID NO: 7	398 (firmus)	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGGTGCTGTCAGTCACATCGC TGTGGCGATGCCGTCAGCAAAAGCCGCT GAACACAATCCAGTTGTTATGGTTACGGTAT CGGAGGAGCTTCATACAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATCGGTTGATTTGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCACGATTGTGCAAAAGGTTTAGACGAA ACGGGTGCGAAAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCAGAACACACTTACTACA TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCCTT GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAAGATTTATACACATCCATTAC AGCAGTGCCGATATGATTGTATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGCTCAAA TTCATGGCGTTGGGCACATTGGTTATTGATG

		AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGAGGCCACAATACAAATTAA
SEQ ID NO: 8	393 (badius)	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTGCGATGCCGTCAAGAAAAGCCGCT GAACACAATCCAGTCGTTATGGTTCACGGTAT CGGAGGAGCTTCATACAATTTCGGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCACGG GGCAAGCTGTATGCAGGGTGTATTGGGACAA GACAGGGACGAATTATAACAATGGCCCGGTAT TATCAGCAGTTGTGCAAAAGGTTAGACGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGTGGCGCAACACACTTTACTACA TAAAAAAATCTGGACGGCGGAAATAAAATTGAA AACGTCGTAACGCTTGGCGCGAACCGTT GACGACAAGCAAGGCCTCCGGGAACAGATC CAAATCAAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTACTT ATCAAAATTAGACGGTGCTAAAACGTTCAA TTCATGGCGTTGGGACATTGGTTATTGATG AACAGCCAAGTCAACAGCCTGATTAAAGAAGG ACTGAACGGCGGAGGCCACAATACAAATTAA
SEQ ID NO: 9	Dc5h	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTGCGTTGCAACCCTCAAGAAAAGCCGCT GAACACAATCCAGTCGTTATGGTTCACGGTAT TGGAGGGGCATTCATTCAATTTCGGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCG GACAAGCTGTATGCAGTTGATTCAAGGACAA GACAGGCACAAATTATAACAATGGCCCGGTAT TATCAGCAGTTGTGCAAAAGGTTAGATGAA ACGGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGGGGGCGCAACACACTTTACTACA TAAAAAAATCTGGACGGCGGAAATAAGTTGAA AACGTCGTAACGCTTGGCGCGAACCGTT GACGACAGGCAAGGCCTCCGGGAACAGATC CAAATCAAAAGATTATACACATCCATTAC AGCAGTGCCGATATGATTGTCATGAATTATT ATCAAGATTAGATGGTGCAGAAACGTTCAA TCCATGGCGTTGGACACATCGGCCTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAAGAAGG GCTGAACGGCGGGGCCTCAATACAAATTAA
SEQ ID NO: 10	Dc5f	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTGCGTTGCAACCCTCAAGAAAAGCCGCT GAACACAATCCAGTCGTTATGGTTCACGGTAT TGGAGGGGCATTCATTCAATTTCGGGAATTA

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		AGAGCTACCTCGTATCTCAGGGCTGGTCGC GACAAGCTGTATGCAGTTGATTCTAAGACAA AACAGGAAATAACCGCAACAATGGTCCCGC TATCGAGATTCGTCAAAGATGTGTTAGACAAA ACGGGTGCCAAAAAGTAGATATTGTGGCTCA TAGTATGGGTGGAGCGAACACGCTATACTATA TCAAGAATCTAGATGGCGGCATAAAATTGAG AACGTGTCAAAATTGGTGGAGCAAACGGACT CGTTCAAGCAGAGCATTACCAGGCACAGATC CAAATCAAAAATTCTTACACATCCGTCTAT AGCTCAGCAGATCTTATTGTCGTCAACAGCCT CTCTCGTTAATTGGCGCAAGAACATCCTGA TCCATGGCGTTGGTCATATCGGTCTATTAACC TCAAGCCAAGTGAAAGGGTATATTAAAGAAGG ACTGAACGGCGGAGGCCTCAATACAAATTAA
SEQ ID NO: 11	Dc5c1	ATGAAAGTGATTTGTTAAGAAAAGGAGTTT GCAAATTCTGTTGCCCTTGCTTAGTGCTAG GTTCAATAGCCTTCATCCAGCCGAAAGAAC AAAGCGGCTGAGCATAATCCGGTTGTAATGGT GCATGGCATGGGTGGTGCCTTATAACTTG CTTCGATCAAACGATACTTAGTATCACAGGGA TGGGATCAAACCAACTTTTGCATCGATTT CATAGACAAAACAGGCAATAACCTAAACAATG GCCCGAGGCTCTCGAGATTGTCGAAAGACGTA CTAGCCAAAACGGGCGCCAAAAAGTAGATAT TGTGGCTCATAGTATGGCGGTGCGAACACGT TATACTATATTAAAAACCTAGACGGTGGAGAT AAAATTGAAAACGTCGTACATTAGGTGGAGC AAACGGACTCGTATCACTCAGAGCATTACAG GCACCGATCCAAATCAAAAATTCTTACACA TCTGTCTATAGCTCAGCCGATCTCATGTC CAACAGCCTTCGCGTTAATTGGCGCAAGAA ACGTCCGTATCCACGGCGTGGACATATCGGT CTATTAACCTCAAGCCAAGTCAAAGGCTATGT GAAAGAAGGATTGAATGGCGGGGACAGAATA CAAATTAA
SEQ ID NO: 12	Dc5a2	ATGAAAGTGATTTGTTAAGAAAAGGAGTTT GCAAATTCTGTTGCTGCATTGGTGTGG GTTCAATGGCCTTCATCCAGCCAAAGAGATC AGAGCGGCTGAGCATAATCCGGTTGATGGT ACATGGCATGGCGGTGCCTTATAACTTG CTTCGATTTAAAGTTACTGGTATCACAGGA TGGGATCGAAACCAATTATTGCTATCGATTT CATAGACAAAACAGGTATAACCGCAACAATG GTCCCGGTCTATCCAGATTGTCGAAAGATGTG CTAGCCAAAACAGGTGCCAAAAAGTTGATAT TGTGGCTCATAGTATGGCGGAGCGAACACGT

100-130-333-000

		TATACTATATTAAGAATCTAGACGGCGGCGAT AAAATAGAAAACGTTTACACTTGGTGGAGC GAACGGACTCGTTCACTCAGAGCATTACCAG GCACCGATCCAAATCAAAAAATCCTTACACA TCCGTCTACAGCTCAGCCGATCTTATCGTCGT CAACAGCCTCTCGCGTTAATTGGCGAAGAA ACGTCCCTCATTCACGGCGTTGGTCACATCGGT CTATTAGCTCAAGCCAAGTCAAAGGCTATAT CAAAGAAGGACTGAATGGCGGAGGCCAAAATA CAAATTAA
SEQ ID NO: 13	Dc512	ATGAAAGTGTATTTGTTAAGAAAAGGAGTTT GCAAATTCTCATTCGCGCTTGCAATTGGTGATTG GTTCAATGGCGTTTATCCAGCCGAAAGAGGCG AAGGCGGCTGAGCATAATCCGGTTGTGATGGT GCATGGCATTGGCGGTGCCTCTTATAACTTTT TTTCTATTAAAAGTTATTTGGCCACACAAGGC TGGGATCGAAACCAATTATATGCTATTGATT CATAGACAAAACAGGAATAACCGCAACAATG GTCCCGGTCTATCGAGATTGTCAAAGATGTG TTAGACAAAACGGGTGCCAAAAAAGTAGATAT TGTGGCTCATAGTATGGGTGGAGCGAACACGC TATACTATATCAAGAATCTAGATGGCGGCGAT AAAATTGAGAACGTTGTCACAATTGGTGGAGC AAACGGACTCGTTCAAGCAGAGCATTACCAG GCACAGATCCAAATCAAAAAATTCTTACACA TCCGTCTATAGCTCAGCAGATCTTATTGTCGT CAACAGCCTCTCAGTTAATTGGCGAAGA AACATCCTGATCCAGGCCTGGTCATATCGGT CTATTACCTCAAGCCAAGTGAAGGGTATAT TAAAGAAGGACTGAACGGCGGAGGCCCTAATA CAAATTAA
SEQ ID NO: 14	Sga	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAAACAATTGTGATGCTGTCTGTTACATCGC TGTTGCGTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTTACGGTAT TGGAGGGGCATCATTCAATTGGGAAATTA AGAGCTATCTCGTATCTCAAGGCTGGCGCG GACAAGCTGTATGCAGTTGATTTCAGGGACAA GACAGGCAATAACTTAAACAACGGTCCAGTAT TATCGCGTTCTGTAAAAAGGTATTAGATGAA ACCGGTGCGAAAAAAGTGGATATTGTCGCTCA CAGCATGGCGCGCTAACACGCTTACTACA TAAAAAAATTGGATGGCGTAATAAAATTGAA AACGTCGTAACACTTGGCGCGGAATCGTCT TGTGACAGGCAAGGCGCTCCGGGTACTGATC CCAACCAAAAGATCTTGTACACATCCGTTAC AGTAGTGCTGATATGATTGTTATGAATTACTT

		AACAAAATTAGACGGGCTAAAATGTTCAA TTCATGGTGTGGACATATCGGCCTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAGAAGG GCTTAACGGCGGAGGCCTCAATACAAATTAA
SEQ ID NO: 15	Sgc	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTGCGTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGCATCATTCAATTTGCGGAAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCG GACAAGCTGTATGCAGTTGATTCTGGGATAA GACAGGCAATAACTAAACAACGGTCCAGTAT TATCGCGTTTGTGAAAAAGGTATTAGATGAA ACCGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGCGCGCTAACACGCTTACTACA TAAAAAAATTGGATGGCGGTAAATAAAATTGAA AACGTCGTAACACTGGCGCGCGAACATCGTCT TGTGACAGGCAAGGCCTCCGGTACTGATC CCAACCAAAAGATATTGTACACATCCGTTAC AGTAGTGCTGATATGATTGTTATGAATTACTT ATCAAAATTAGACGGGCTAAAATGTTCAA TTCATGGTGTGGACATATCGGCCTCTGTAC AGCAGCCAAGTCAATAGCCTGATTAAGAAGG GCTTAACGGCGGAGGACTCAATACGAATTAA
SEQ ID NO: 16	Sgd	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTGCGTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGCATCATTCAATTTGCGGAAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCG GACAAGCTGTATGCAGTTGATTAGTACAA AACAGGCAATAACTAAACAACGGTCCAGTAT TATCGCGTTTGTGAAAAAGGTATTAGATGAA ACCGGTGCGAAAAAGTGGATATTGTCGCTCA CAGCATGGCGCGCTAACACGCTTACTACA TAAAAAAATTGGATGGCGGTAAATAAAATTGAA AACGTCGTAACACTGGCGCGAACATCGTCT TGTAAACAGGCAAGGCCTCCGGTACTGATC CCAACCAAAAGATCTTGTACACATCCGTTAC AGTAGTGCTGATATGATTGTTATGAATTACTT ATCAAAATTAGACGGGCTAAAATGTTCAA TTCATGGTGTGGACATATCGGCCTCTGTAC AGCAGCCAAGTCAACAGCCTGATTAAGAAGG GCTTAACGGCGGGGCGTAATACGAATTAA
SEQ ID NO: 17	Sgf	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCTGTTACATCGC TGTTGCGTTGCAACCGTCAGCAAAAGCCGCT

		GAACACAATCCAGTCGTTATGGTTACGGTAT TGGAGGGGCATCATTCAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTCAAAGACAA GACAGGAAATAACCGCAACAATGGTCCCGTC TATCGAGATTCGTCAAAGATGTGTTAGACAAA ACAGGAGCCAAAAAAGTAGATATTGTGGCTCA TAGTATGGCGGAGCGAACACATTATACTATA TTAAGAATCTAGATGGTGGCGATAAAATTGAG AACGTGTCACAATTGGTGGAGCAAACGGACT CGTTCAAGCAGAGCATTACCAGGCACAGATC CAAATCAAAAATTCTTACACATCCGTCTAT AGCTCAGCAGATCTTATTGTCGTCAACAGTCT CTCTCGTTAATTGGCGCAAGAACGTCCAAA TCCATGGCGTTGGACATATCGGTCTATTAAACC TCAAGCCAAGTCAAAGGATATATTAAAGAAGG ACTGAACGGCGGGGCCAAATACAAATTAA
SEQ ID NO: 18	Sgh	ATGAAATTGTAAAAAGAAGGATCCTTGCACT TGTAACAATTTCGATGCGTCTGTTACATCGC TGTTGCGTTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTTACGGTAT TGGAGGGGCATCATTCAATTTCGCGGAATTA AGAGCTATCTCGTATCTCAGGGCTGGTCGCGG GACAAGCTGTATGCAGTTGATTTCATTGACAA GACAGGAAATAACCGCAACAATGGTCCCGTC TATCGAGATTCGTCAAAGATGTGTTAGACAAA ACAGGAGCCAAAAAAGTAGATATTGTGGCTCA TAGTATGGCGGAGCGAACACATTATACTATA TTAAGAATCTAGATGGTGGCGATAAAATTGAG AACGTGTCACAATTGGTGGAGCAAACGGACT CGTTCAAGCAGAGCATTACCAGGCACAGATC CAAATCAAAAATTCTTACACATCCGTCTAT AGCTCAGCAGATCTTATTGTCGTCAACAGTCT CTCTCGTTAATTGGCGCAAGAACGTCCAAA TCCATGGCGTTGGACATATCGGTCTATTAAACC TCAAGCCCTAGTCAAAGGATATATTAAAGAAGG ACTGAACGGCGGAGGCCAAATACAAATTAA
SEQ ID NO: 19	Mt2b1	ATGAAAGTGATTTGTTAAGAAAAGGAGTTT GCAAATTCTGTTGCCCTTGCCTTAGTGATAG GTTCAATGCCCTTCATCCAGCCAAAGAAATC AAAGCAGCTGAGCACAAATCCGTTGTGATGGT ACATGGTATTGGAGGAGCGTCTATAACTTG CTTCGATTAAAAGTTATTGGTTAACCAAGGC TGGGATCGAAACCAATTATTGCTATCGATTT CATAGACAAAACAGGGAAATAACCGCAACAATG GTCCTCGTTATCTAGATTGTCGTCAAAGATGTG CTAGACAAAACGGGTGCCAAAAAAGTAGATAT

		TGTGGCGCATAGTATGGCGGGCGAACACGC TATACTATATTAAGAATCTAGATGGCGGCAT AAAATTGAAAACGTCGTCACCATTGGTGGAGC AACGGACTCGTTCACTCAGAGCATTACAG GAACAGATCCAATCAAAAAATTCTCTATACA TCTGTCCTAGCTCAGCCGATTGATTGTCGT CACACGCCTTCGCGTTAACTGGCGCAAGAA ATGTCCTGATCCACGGCGTGGCCATATCGGT CTATTAACCTCAAGCCAAGTGAAAGGGTATAT TAAAGAAGGACTGAACGGCGGGGCTAAATA CAAATAA
SEQ ID NO: 20	H2a	ATGAAATTGTAAAAAGAAGGATCATTGCACT TGTAACAATTTGATGCTGTCGTTACATCGC TGTTTGCCTGCAACCGTCAGCAAAAGCCGCT GAACACAATCCAGTCGTTATGGTCACGGTAT TGGAGGGCATCATTCAATTTGCGGGAATTA AGAGCTATCTGTATCTCAGGGCTGGTCGCG GACAAGCTGTATGCAGTTGATTTCAGGGACAA GACAGGAAATAACCGCAACAATGGTCCGCGTC TATCTAAATTCTGTCAAAGATGTGTTAGACAAA ACGGGTGCCAAAAAAGTAGATATTGTGGCTCA TAGTATGGCGGGCGAACACGCTATACTATA TTAAGAATCTAGATGGCGCGATAAAATTGAG AACGTTGTACAATTGGCGGAGCAAACGGACT CGTTCAAGCAGAGCATTACCAAGGCACAGATC CAAATCAAAAATTCTTACACATCCGTCTAC AAGCTCAGCCGATCTCATTGTCGTCAACAGTC TCTCTCGTTAATTGGCTGCAAGAACAGTCC AAATCCATGGCGTTGGACATATCGGTCTATTA ACCTCAAGCCAAGTCAAAGGATATATTAAAGA AGGACTGAACGGCGGGGACTAAATAACAAATT AA
SEQ ID NO: 21	1f15(G2)	TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGCATCATTCAATTTGCGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGGCAAGCTGTATGCGGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGT TTATCGCGTTTGTGAAAAAGGTATTAGATGA AACGGTGCAAAAAAGTGGATATTGTCGCTC ACAGCATGGCGCGCTAACACGCTTACTAC ATAAAAATCTGGACGGCGGAAATAAGTTGA AACGTCGTAACGCTTGGCGGCACGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGTAAAGATGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT

TACCTCGTGTGGCACATTGGTTATTGAT

		GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGACTCAATACGAATTGA
SEQ ID NO: 22	3C12	TGAACACAATCCAGTTGTTATGGGTCACGGTA TTGGAGGGGCATCATTCAATTTGCGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCTAGATTCTCGTCAAAGATGTGCTAGACAA AACGGGTGCGAAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AAACGTCGTAACGCTTGGCGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAAGATTTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCAATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGACTCAATACGAATTGA
SEQ ID NO: 23	3N19(G2)	TGAACACAATCCAGTTGTTATGGGTCACGGTA TTGGAGGGGCATCATTCAATTTGCGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTTTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAAGGTATTAGATGA AACCGGTGCGAAAAAAGTGGACATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AAACGTCGTAACGCTTGGCGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAAGATTTTATACACATCCATTAA CGGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATCCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGACTGAATACAAATTGA
SEQ ID NO: 24	G2.2	TGAACACAATCCAGTTGTTATGGGTCACGGTA TCGGAGGGGCATCATTCAATTTGCGGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAGGTTTAGACGA AACGGGTGCGAAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AAACGTCGTAACGCTTGGCGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT

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SEQ ID NO: 25	2C3	TGAACACAATCCAGTTGTTATGGTCACGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGGCAAGCTGTATGCGGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAGGTTTAGACGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGCGCGCGAACACACTTACTAC ATAAAAAAATTGGATGGCGGTAAATAAAATTGA AACAGTCGTCACCATTGGTGGAGCAAACGGAC TCGTTCAAGCAGAGCATTACCAAGGCACAGAT CCAAATCAAAAATTCTTACACATCCGTCTA TAGCTCAGCAGATCTTATTGTCGTCAACAGTC TCTCTCGTTAATTGGCGCAAGAAACGTCAA ATCCATGGCGTTGGACATATCGGTCTATTAAAC CTCAAGCCAAGTCAAAGGATATATTAAAGAAG GGCTTAACGGCGGGGCCACAATACGAATTGA
SEQ ID NO: 26	2F11	TGAACACAATCCAGTTGTTATGGTCACGGTA TCGGAGGGAGCTTCATACAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAGGTTTAGACGA AACCGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTACTAC ATAAAAAACTGGACGGCGGAATAAAATTGA AACAGTCGTAACGCTTGGCGCGCGAACCGTT TGACGACAAGCAGGGCGCTCCGGGAACAGAT CCAAATCAAAAGATTTATACACATCCATT CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTACAA ATTCATGGCGTTGGCACATTGGTTATTGAT GAACAGCCAAGTCAAAGGATATATTAAAGAAG GACTGAACGGCGGGAGGCCTAAATACGAATTGA
SEQ ID NO: 27	KV11(6C7)	TGAACACAATCCAGTTGTTATGGTCACGGTA TTGGAGGGGCATCATTCAAGTTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATCCGGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAGGTTGGACGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC

0960563 - 02406

		ACAGTATGGTGGCGCAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCCTTGAT TGACGACAAGCAAGGCCTCCGGGTACTGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGCTGATATGATTGTTATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCATGGCGTGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCTAAATACAAATTGA
SEQ ID NO: 28	KV6(3A1)	TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGGCATCATTCACTTGCCTGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTGGACAA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTGGACGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGTATGGTGGCGCAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCCTTGAT TGACGACAAGCAAGGCCTCCGGGTACTGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGCTGATATGATTGTTATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCATGGCGTGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCTAAATACAAATTGA
SEQ ID NO: 29	KV2(2D1)	TGAACACAATCCAGTTGTTATGGTTACCGTA TCGGAGGGAGCTTCATACAGTTGCCTGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTGGACAA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTAGACGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGTGGCGCAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCCTTGAT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCATGGTGTGGACATATCGGCCTCTGTA CAGCAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCTAAATACAAATTGA
SEQ ID NO: 30	N2.5	TGAACACAATCCAGTTGTTATGGTTACCGTA TCGGAGGGAGCTTCATACAGTTGCCTGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG

DNA Sequencing

		GGGCAAGCTGTATCGGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAGGTTTAGACGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGCGCGAACACACTTACTAC ATAAAAAACTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACGTAT CCCACCAAAAGATCTGTACACATCCGTTA CAGTAGTGCTGATATGATTGTTATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCATGGCGTGGGCACACTGGTTATTGAT AACAGCCAAGTCAACAGCCTGATTAAAGAAG GAACGCGGGGCCACAATACAAATTGA
SEQ ID NO: 31	KV5(2H6)	TGAACACAATCCAGTTGTTATGGTTACGGTA TTGGAGGGAGCATCATAAATTTCGGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATACGGTTGATTTGGGACA AGACAGGCACAAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAGGTTTAGACGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAACTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT TTGTAACAGGCAAGGCCTCCGGGAACAGAT CCCACCAAAAGATTTGTACGCATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGGCTAAAAACGTTCAA ATTCATGGCGTGGGCACACTGGTTATTGAT AACAGCCAAGTCAACAGCCTGATTAAAGAAG GAACGCGGGGCCCTGAATACAAATTGA
SEQ ID NO: 32	3E5	TGAACACAATCCAGTCGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTTCGGGAATT AGGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATCGGGTTGATTTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAGGTTTAGATGA AACCGGTGCAGAAAAAGTGGACATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAACTGGACGGCGGAATAAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCCACCAAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGGCTAAAAATGTTCAA ATTCCATGGCGTGGACACATCGGCCTCTGTA CAGCAGCCAAGTCAACAGCCTGATTAAAGAAG

		GACTAACGGCGGGGCCTCAATACGAATTGA
SEQ ID NO: 33	G2.1	TGAACACAATCCAGTTGTTATGGTTACCGTA TCGGAGGGGCATCATTCAATTTGCGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTTAGACGA AACCGGTGCGAAAAAGTGGACATTGTCGCTC ACAGCATGGCGCGCTAACACGCTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AACGTCGTAACGCTTGGCGGACGAACCGTT TGACGACAAGCAGGGCGCTCCGGGAAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAACTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTAACGGCGGGGACTCAATACGAATTGA
SEQ ID NO: 34	3H24(G2)	TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGGCATCATTCAATTTGCGGAAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCCGTATGCGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTTAGACAA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AACGTCGTAACGCTTGGCGGCGAACCGTT TGACGACAAGCAGGGCGCTCCGGGAAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTAACGGCGGGGACTCAATACGAATTGA
SEQ ID NO: 35	KV10(4G6)	TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGGCATCATTCAATTTGCGGAAATT AAGAGCTATCTCGTGTCTCAGGGCTGGCCGCG GGACAAGCTGTATGCGAGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTTAGACGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AACGTCGTAACACTTGGCGGCGAACCGTC TTGTAACAGGCAAGGCCTCCGGGAACTGAT CCCAACCAAAGATTTATACACATCCATTAA

TACGATGGCTGGCACATTGGTTATTGAT

		CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTCGGACATATCGGCCTCTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACACGGGGGCCACAATACAAATTGA
SEQ ID NO: 36	KV12(6D4)	TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAAGTTGCGGGAAATT AGGAGCTATCTCGTATCTCAGGGCTGGCCCGCG GGACAAGCTGTATGCGGTTGATTGGGACA AGACAGGCACAAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAGGTATTAGATGA AACCGGTGCGAAAAAGGGATATTGTCGCC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AACCGTCGTGACGCTTGGCGCGGCCAACCGTT TGACGACAGGCAAGGCCTCCGGGTACTGAT CCCAATCAAAAGATTGATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAAGAAG GAUTGAACACGGGGAGGCCACAATACAAATTGA
SEQ ID NO: 37	N2.2	TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAAGTTGCGGGAAATT AGGAGCTATCTCGTATCTCAGGGCTGGCCCGCG GGACAAGCTGTATGCGGTTGATTGGGACA AGACAGGCACAAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAGGTATTAGATGA AACCGGTGCGAAAAAGGGATATTGTCGCC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AACCGTCGTGACGCTTGGCGCGGCCAACCGTT TGACGACAGGCAAGGCCTCCGGGTACTGAT CCCAATCAAAAGATTGATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAAGAAG GAUTGAACACGGGGAGGCCACAATACAAATTGA
SEQ ID NO: 38	N2.3	TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGGGGGGCATCATTCAAGTTGCGGGAAATT AGGAGCTATCTCGTATCTCAGGGCTGGCCCGCG GGACAAGCTGTATGCGGTTGATTGGGACA AGACAGGCACAAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAGGTATTAGATGA AACCGGTGCGAAAAAGGGATATTGTCGCC ACAGCATGGGTGGCGCGAACACACTTACTAC

		ATAAAAAAATCTGGACGGCGGAAATAAGTTGG AACGTCGTGACGCTTGGCGGCCAACCGTT TGACGACAGGCAGGGCCTCCGGGTACTGAT CCCAATCAAAGATTTATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAAGAAG GACTGAACGGCGGAGGCCACAATACAAATTGA
SEQ ID NO: 39	N2.1	TGAACACAATCCAGTTGTTATGGTCACGGTA TCGGAGGGGACATCATTCAATTTCGCGGGATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGACAAGCTGTATGCGGTTGATTTGGGACA AGACAGGCACAAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTATTAGATGA AACCGGTGCGAAAAAAGTGGATATTGTCGCCC ACAGCATGGTGGCGCGAACACACTTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAGTTGA AACGTCGTGACGCTTGGCGGCCAACCGTT TGACGACAGGCAGGGCCTCCGGGTACTGAT CCCAATCAAAGATTTATACACATCCGTTA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGGCTGATTAAAGAAG GACTGAACGGCGGAGGCCACAATACAAATTGA
SEQ ID NO: 40	KV4(2E12)	TGAACACAATCCAGTTGTTATGGTCACGGTA TTGGAGGGACATCATTCAATTTCGCGGGATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGACAAGCTGTATGCGGTTGATTTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAAGGTTTAGACGA AACGGGTGCGAAAAAAGTGGATATTGTCGCTC ACAGCATGGCGCGAACACGCTTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AACGTCGTGACGCTTGGCGGCCAACCGTT TGACGACAAGCAAGGCAGGGCTCCGGGAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCCACAATACAAATTGA
SEQ ID NO: 41	KV9(4C6)	TGAACACAATCCAGTTGTTATGGTCACGGTA TCGGAGGGGACATCATTCAATTTCGCGGGATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGACAAGCTGTATGCGAGTTGATTTAGTGACA

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		AAACAGGCACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGTTTAGACGA AACGGTGCAAAAAAGGGATATTGTCGCTC ACAGCATGGGGGCGCGAACACACTTACTAC ATAAAAAATCTGGATGGCGGTAAATAAAATTGA AACGTCGTAACACTTGGCGGCGGAACCGTT TGACGACAAGCAAGGCCTCCGGGTACTGAT CCCAACCAAAAGATCTTGTACACATCCATT CAGCAGTGCGATATGGTTGTATGAATTACT TATCAAATTAGACGGGCTAAAATGTTCAA ATTCATGGTGTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGGGGGCCACAATACGAATTGA
SEQ ID NO: 42	7D6	TAAACACAATCCAGTTATGGTTACGGTA TTGGAGGGGCATCATAACATTGCGGAAATA AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTAGTGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGTTTAGACGA AACGGTGCaaaaAAGGGATATTGTCGCTC ACAGCATGGGGGCGCGAACACACTTACTAC ATAAAAAATCTGGACGGCGGTAAATAAAATTGA AACGTCGTAACACTTGGCGGCGGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATTATACACATCCATT CAGCAGTGCGATATGATTGTATGAATTACT TATCAAATTAGACGGGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGGGGGGATTAAATACGAATTGA
SEQ ID NO: 43	3F3	TGAACACAATCCAGTTATGGTTACGGTA TTGGAGGGGCATCATTCAATTGCGGAAATT AAGAGCTATCTCGAATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCAGTTGATTGGACA AGACGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGCAAAAGGCTTAGACGA AACGGTGCaaaaAAGGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTACTAC ATAAAAAATCTGGACGGCGGAAATAAAATTGA AACGTCGTAACGCTTGGCGGCGGAACCGTT TGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATTATACACATCCATT CAGCAGTGCGATATGATTGTATGAATTACT TATCAAATTAGACGGGCTAAAACGTTCAA ATTCCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGGGGGGATTAAATACGAATTGA

DNA sequence - 03/2020

SEQ ID NO: 44	2D11(G2)	TGAACACAATCCAGTTGTTATGGTTACCGTA TCGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAAGGTATTAGATGA AACCGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGGCGCGAACACACTTTACTAC ATAAAAAACTGGACGGCGGAATAAAATTGA AACAGTCGTACACTTGGCGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTAACGGCGGGGCCAACATCGAATTGA
SEQ ID NO: 45	3C23(G2)	TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAGGTTTAGACGA AACGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTTACTAC ATAAAAAACTGGACGGCGGAATAAAATTGA AACAGTCGTACACTTGGCGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTAACGGCGGGGCCAACATCGAATTGA
SEQ ID NO: 46	G2.3	TGAACACAATCCAGTCGTTATGGTTACCGTA TTGGAGGGGCATCATTCAATTTCGCGGAATA AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTGGGACA GGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGCAAAGGTTTAGACGA AACGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGGTGGCGCGAACACACTTTACTAC ATAAAAAACTGGACGGCGGAATAAAATTGA AACAGTCGTACGCTTGGCGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTGCT

		TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTTATTGAT GAACAGCCAAGTCAACACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCCAGAATACGAATTGA
SEQ ID NO: 47	2A3	TGAAACACAATCCAGTTGTTATGGTTACCGGTA TTGGAGGGGCATCGTTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTCAAAGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAAGGTATTAGATGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGCGCGCTAACACGCTTACTAC ATAAAAAGATCTGGACGGCGGAATTAAATTGA AACGTCGTAACGCTTGGCGCGAACCCT CGACGACAAGCAAGGCCTCCGGGTACTGAT CCCAACCAAAAGATCTTGTACACATCCGTTA CAGTAGTGCTGATATGATTGTATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTTATTGAT GAACAGCCAAGTCAACACAGCCTGATTAAAGAAG GACTGAACGGCGGAGGCCAAATACAAATTGA
SEQ ID NO: 48	2F4	TGAACACAATCCAGTTGTTATGGTTACCGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAAGGTATTAGATGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGTGCGCTAACACGCTTACTAC ATAAAAATCTGGACGGCGCGATAAAATTGA AACGTCGTAACACTTGGCGCGCGAACCCT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATCTTGTACACATCCGTTA CAGTAGTGCTGATATGATTGTATGAATTACT TATCAAAATTAGACGGTGCTAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTTATTGAT GAACAGCCAAGTCAACACAGCCTGATTAAAGAAG GGCTGAACGGCGGAGGCCAGAATACGAATTGA
SEQ ID NO: 49	2B9(G2)	TGAACACAATCCAGTTGTTATGGTTACCGGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCAGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCGCGTTTGTGAAAAAGGTATTAGATGA AACGGTGCAGAAAAAGTGGATATTGTCGCTC ACAGCATGGGGCGCGAACACACTTACTAC ATAAAAATCTGGACGGCGGAATAAAATTGA

09060666-071301

		AAACGTCGTAAACACTTGGCGGCGGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACAGAT CCAAATCAAAGATTATACACATCCATT CAGCAGTGCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGGCTAAAATGTTCAA ATTCATGGCGTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACGGCGGAGGCCAAAATACGAATTGA
SEQ ID NO: 50	2C5	TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGAGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGTA TTATCGCGTTTGTGAAAAAGGTATTAGATGA AACGGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGCGCTAACACGCTTACTAC ATAAAAAAATCTGGATGGCGGTAAATAAAATTGA AAACGTCGTACACTTGGCGGCGGAACCGTT CGACGACAAGCAAGGCCTCCGGGAACGTGAT CCCAACCAAAAGATTATACACATCCATT CAGCAGTGCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCCTAAAACGTTCAA ATTCATGGCGTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GAUTGAACGGCGGAGGCCAAAATACGAATTGA
SEQ ID NO: 51	KV1(2A6)	TGAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGGTGATTCAAGGACA AGACAGGCACAAATTATAACAATGGCCCGTA TTATCACGATTGTGAAAAAGGTATTAGATGA AACCGGTGCGAAAAAGTGGATATTGTCGCTC ACAGCATGGCGGCGCTAACACGCTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAAATTGA AAACGTCGTACGCTTGGCGGCGGAACCGTT CGACGACAAGCAAGGCCTCCGGGTACTGAT CCCAACCAAAAGATTATACACATCCATT CAGCAGTGCGATATGATTGTCATGAATTACT TATCAAAATTAGACGGTGCCTAAAACGTTCAA ATTCATGGCGTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTTAACGGCGGGGCCAGAATACGAATTGA
SEQ ID NO: 52	2D13(G2)	TAAACACAATCCAGTTGTTATGGTTACCGTA TTGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACGAGCTGTATGCGGGTGATTGGGACG AGACAGGGACGAATTATAACAATGGCCCGTA

		TTATCACGATTGTGAAAAGGTTTAGACGA AACCGGTGCAAAAAGGGATATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAATTGA AACGTCGTAACGCTTGGCGCGAACCGTT CGACGACAAGCAAGGCCTCCGGGTACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGTAAAAATGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTGAACGGCGGAGGCCAAAATACGAATTGA
SEQ ID NO: 53	3C8	TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCGCG GGACAAGCTGTATGCGGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGAAAAGGTTTAGACGA AACGGGTGCAAAAAGGGATATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAATTGA AACGTCGTAACACTTGGCGCGCGAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGTAAAAACGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GACTGAACGGCGGGGCCAAAATACAAATTGA
SEQ ID NO: 54	2D5	TGAACACAATCCAGTTGTTATGGTTACGGTA TCGGAGGGGCATCATTCAATTTCGCGGAATT AAGAGCTATCTCGTATCTCAGGGCTGGTCACG GGGCAAGCTGTATGCGGTTGATTGGGACA AGACAGGGACGAATTATAACAATGGCCCGGTA TTATCACGATTGTGAAAAGGTTTAGACGA AACGGGTGCAAAAAGGGATATTGTCGCTC ACAGCATGGTGGCGCGAACACACTTACTAC ATAAAAAAATCTGGACGGCGGAAATAAATTGA AACGTCGTAACACTTGGCGCGCGAACAGAT CCAAATCAAAGATTTATACACATCCATTAA CAGCAGTGCCGATATGATTGTCATGAATTACT TATCAAATTAGACGGTGTAAAAATGTTCAA ATTCATGGCGTTGGGCACATTGGTTATTGAT GAACAGCCAAGTCAACAGCCTGATTAAAGAAG GGCTGAACGGCGGAGGCCAAAATACAAATTGA

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SEQ ID NO: 55	405 (pumilus)	MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLRFVQKVLDE TGAKKVDIVAHSMGGANTPYYIKNLDGGNKIE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNAQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 56	406 (subtilis)	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWDKTGTNYNNGPVLPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVA NVVTLGGANRLTTGKALPGTDPNQKILYTSIY SSADMIVVINYLSSRLDGARNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 57	402 (megaterium)	MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA DTIQLLWFTGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHINTN
SEQ ID NO: 58	400 (lentus)	MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 59	396 (circulans)	MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 60	392 (azotoformans)	MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GELYAVDFWDKTGTNYNNGPVLRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSANMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLDTN
SEQ ID NO: 61	398 (firmus)	MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY

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		SSADMIVMNYLSKLDGAKNAQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN
SEQ ID NO: 62	393 (badius)	MKFVKRRIIALVTILVLSVTSLFAMQPSAKAA EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSPRFVQVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN
SEQ ID NO: 63	Dc5h	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFDKDTGTNYNNGPVLSPRFVQVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTGKALPGTDPNQKILYTSIY SSADMIVMNYLSRLDGARNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 64	Dc5f	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDXDKDTGNRNNNGPRLSRFVKDVLDK TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNILIHGVGHIGLLT SSQVKGYIKEGLNGGGLNTN
SEQ ID NO: 65	Dc5c1	MKVIFVKKRSLQILVALALVLGSIAFIQPKEA KAAEHNPVVMVHGMMGGASYNFASIKRYLVSQG WDQNQLFAIDFIDKTGNLNNNGPRLSRFVKDV LAKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIENVVTLGGANGLVSLRALPGTDPNQKILYT SVYSSADLIVVNSLSRLIGARNVLIHGVGHIG LLTSSQVKGYIKEGLNGGGQNTN
SEQ ID NO: 66	Dc5a2	MKVIFVKKRSLQILVVLALVMGSMAFIQPKEI RAAEHNPVVMVHGMMGGASYNFASIKSYLVSQG WDRNQLFAIDFIDKTGNRNNNGPRLSRFVKDV LAKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIENVVTLGGANGLVSLRALPGTDPNQKILYT SVYSSADLIVVNSLSRLIGARNVLIHGVGHIG LLASSQVKGYIKEGLNGGGQNTN
SEQ ID NO: 67	Dc512	MKVIFVKKRSLQILIALALVIGSMAFIQPKEA KAAEHNPVVMVHGIGGASYNFFSIKSYLATQG WDRNQLYAIDFIDKTGNLNNNGPRLSRFVKDV LDKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIENVVTIGGANGLVSSRALPGTDPNQKILYT SVYSSADLIVVNSLSQFNWRKKHPDPGVGHIG LLTSSQVKGYIKEGLNGGGLNTN
SEQ ID NO: 68	Sga	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFRDKTGNLNNNGPVLSPRFVKVLDE

		TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLVTGKALPGTDPNQKILYTSVY SSADMIVMNYLTKLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGLNTN
SEQ ID NO: 69	Sgc	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWDKTGNLNNNGPVLSRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLVTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGLNTN
SEQ ID NO: 70	Sgd	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFSDKTGNNLNNGPVLSRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLVTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGLNTN
SEQ ID NO: 71	Sgf	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFDKTGNNRNNGPRLSRFVKDVLDK TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNVQIHGVGHIGLLT SSQVKGYIKEGLNGGLNTN
SEQ ID NO: 72	Sgh	MKFVKRRILALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFIDKTGNRNNNGPRLSRFVKDVLDK TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNVQIHGVGHIGLLT SSLVKGYIKEGLNGGQNTN
SEQ ID NO: 73	Mt2b1	MKVIFVKKRSLQILVALALVIGSMAFIQPKEI KAAEHNPVVMVHGIGGASYNFASIKSYL VNQG WDRNQLFAIDFIDKTGNRNNNGPRLSRFVKDV LDKTGAKKVDIVAHSMGGANTLYYIKNLDGGD KIENVVTIGGANGLVSLRALPGTDPNQKILYT SVYSSADLIVVNSLSRLTGARNVLIHGVGHIG LLTSSQVKGYIKEGLNGGLNTN
SEQ ID NO: 74	H2a	MKFVKRRIIALVTILMLSVTSLFALQPSAKAA EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFRDKTGNRNNNGPRLSKFVKDVLDK TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY KLSRSHCRQQSLSFNWLQETVQIHGVGHIGLL TSSQVKGYIKEGLNGGLNTN

SEQ ID NO: 75	1f15(G2)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLLGGTNRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGLNTN
SEQ ID NO: 76	3C12	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGLNTN
SEQ ID NO: 77	3N19(G2)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY GSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGLNTN
SEQ ID NO: 78	G2.2	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY GSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGLNTN
SEQ ID NO: 79	2C3	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTIGGANGLVSSRALPGTDPNQKILYTSVY SSADLIVVNSLSRLIGARNVQIHGVGHIGLLT SSQVKGYIKEGLNGGGHNTN
SEQ ID NO: 80	2F11	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLLTSRALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVKGYIKEGLNGGGHNTN
SEQ ID NO: 81	KV11(6C7)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYPVDFWDKTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLLTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGLNTN
SEQ ID NO: 82	KV6(3A1)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLLTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM

		NSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 83	KV2(2D1)	EHNPVVMVHGIGGASYSFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNNGPVLSPRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 84	N2.5	EHNPVVMVHGIGGASYSFAGIKSYLVSQGWSR GKLYAVDFWDKTGTNYNNNGPVLSPRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHTGLLM NSQVNSLIKEGLNGGGHNTN
SEQ ID NO: 85	KV5(2H6)	EHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR GKLYTVDFWDKTGTNYNNNGPVLSPRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLVTGKALPGTDPNQKILYASVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN
SEQ ID NO: 86	3E5	EHNPVVMVHGIGGASFNFAGIRSYLVSQGWSR GKLYAVDFWDRTGTNYNNNGPVLSPRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLY SSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 87	G2.1	EHNPVVMVHGIGGASFNFAGIRSYLVSQGWSR GKLYAVDFWDKTGTNYNNNGPVLSPRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGTNRLTTSRALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 88	3H24(G2)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKPYAVDFWDKTGTNYNNNGPVLSPRFVQKVLDK TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 89	KV10(4G6)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWPR DKLYAVDFWDKTGTNYNNNGPVLSPRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE SVVTLLGGANRLVTGKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN
SEQ ID NO: 90	KV12(6D4)	EHNPVVMVHGIGGASFNFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNNGPVLSPRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLLGGANRLTTGKALPGTDPNQKILYTSVY

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		SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN
SEQ ID NO: 91	N2.2	EHNPVVMVHGIGGASFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNGPVLSRFVQVLDE TGAKKVDIVAYSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN
SEQ ID NO: 92	N2.3	EHNPVVMVHGIGGASFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNGPVLSRFVQVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVG NVVTLGGANRLTTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN
SEQ ID NO: 93	N2.1	EHNPVVMVHGIGGASFAGIRSYLVSQGWPR DKLYAVDFWDKTGTNYNNGPVLSRFVQVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLGGANRLTTGKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNRLIKEGLNGGGHNTN
SEQ ID NO: 94	KV4(2E12)	EHNPVVMVHGIGGTSFNFAGIKSYLVSQGWSR DKLYAVDFWDKTGTNYNNGPVLSRFVQVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSLIKEGLNGGGHNTN
SEQ ID NO: 95	KV9(4C6)	EHNPVVMVHGIGGASFAGIKSYLVSQGWSR DKLYAVDFSDKTGTNYNNGPVLSRFVQVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSLIKEGLNGGGHNTN
SEQ ID NO: 96	7D6	KHNPVVMVHGIGGASYNFAGIKSYLVSQGWSR DKLYAVDFSDKTGTNYNNGPVLSRFVQVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSLIKEGLNGGGLNTN
SEQ ID NO: 97	3F3	EHNPVVMVHGIGGASFNFAGIKSYLESQGWSR GKLYAVDFWDKTGTNYNNGPVLSRFVKALDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRLTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNLSIKEGLNGGGQNTN
SEQ ID NO: 98	2D11(G2)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE

		NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 99	3C23(G2)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGHNTN
SEQ ID NO: 100	G2.3	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDRTGTNYNNGPVLSPRFVQKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNCLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 101	2A3	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFKDGTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGLNTN
SEQ ID NO: 102	2F4	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWDKTGTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGDKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSVY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 103	2B9(G2)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DKLYAVDFWGKTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 104	2C5	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFWDKTGTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 105	KV1(2A6)	EHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR GKLYAVDFKDGTGTNYNNGPVLSPRFVKKVLDE TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 106	2D13(G2)	KHNPVVMVHGIGGASFNFAGIKSYLVSQGWSR DELYAVDFWDETGTNYNNGPVLSPRFVQKVLDE

		TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 107	3C8	EHNPVVMVHGIGGASFNFAGIKSYLVSGQWSR DKLYAVDFWDKTGTNYNNNGPVLSRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKVE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN
SEQ ID NO: 108	2D5	EHNPVVMVHGIGGASFNFAGIKSYLVSGQWSR GKLYAVDFWDKTGTNYNNNGPVLSRFVQKVLD TGAKKVDIVAHSMGGANTLYYIKNLDGGNKIE NVVTLGGANRSTTSKALPGTDPNQKILYTSIY SSADMIVMNYLSKLDGAKNVQIHGVGHIGLLM NSQVNSLIKEGLNGGGQNTN

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